Granbel

1642

INPUT SET: S3072.raw

> This Raw Listing contains the General
> Information Section and up to the first 5 pages.

```
 1                              SEQUENCE LISTING
 2
 3     (1)      General Information:                    ENTERED
 4            (i) APPLICANT: Lyman, Stewart D.
 5                           Beckmann, M. Patricia
 6
 7            (ii) TITLE OF INVENTION: Ligands for flt3/flk-2 Receptors
 8
 9            (iii) NUMBER OF SEQUENCES: 8
10
11             (iv) CORRESPONDENCE ADDRESS:
12                    (A) ADDRESSEE: Stephen L. Malaska, Immunex Corporation
13                    (B) STREET: 51 University Street
14                    (C) CITY: Seattle
15                    (D) STATE: Washington
16                    (E) COUNTRY: US
17                    (F) ZIP: 98101
18
19             (v) COMPUTER READABLE FORM:
20                    (A) MEDIUM TYPE: Floppy disk
21                    (B) COMPUTER: Apple Macintosh
22                    (C) OPERATING SYSTEM: Macintosh 7.0.1
23                    (D) SOFTWARE: Microsoft Word, Version #5.1
24
25            (vi) CURRENT APPLICATION DATA:
26                    (A) APPLICATION NUMBER:US/08/993,962
27                    (B) FILING DATE:  December 18, 1997
28                    (C) CLASSIFICATION:435
29
30            (vii) PRIOR APPLICATION DATA:
31
32                    (A) APPLICATION NUMBER:US/08/162,407
33                    (B) FILING DATE:  December 3, 1993
34
35                    (A) APPLICATION NUMBER: 08/111,758
36                    (B) FILING DATE:  August 25, 1993
37                    (C) CLASSIFICATION:
38
39            (vii) PRIOR APPLICATION DATA:
40                    (A) APPLICATION NUMBER: 08/106,463
41                    (B) FILING DATE:  August 12, 1993
42                    (C) CLASSIFICATION:
43
44            (vii) PRIOR APPLICATION DATA:
45                    (A) APPLICATION NUMBER:  08/068,394
46                    (B) FILING DATE:  May 24, 1993
```

INPUT SET: S3072.raw

```
47                  (C) CLASSIFICATION:
48
49      (viii) ATTORNEY/AGENT INFORMATION:
50                  (A) NAME: Malaska, Stephen L.
51                  (B) REGISTRATION NUMBER: 32,655
52                  (C) REFERENCE/DOCKET NUMBER: 2813-C
53
54        (ix) TELECOMMUNICATION INFORMATION:
55                  (A) TELEPHONE: (206) 587-0430
56                  (B) TELEFAX: (206) 233-0644
57                  (C) TELEX: 756822
58
59  (2) INFORMATION FOR SEQ ID NO:1:
60
61        (i) SEQUENCE CHARACTERISTICS:
62                  (A) LENGTH: 879 base pairs
63                  (B) TYPE: nucleic acid
64                  (C) STRANDEDNESS: single
65                  (D) TOPOLOGY: linear
66
67       (ii) MOLECULE TYPE: cDNA to mRNA
68
69      (iii) HYPOTHETICAL: NO
70
71       (iv) ANTI-SENSE: NO
72
73       (ix) FEATURE:
74                  (A) NAME/KEY: misc_feature
75                  (B) LOCATION: 1..25
76
77       (ix) FEATURE:
78                  (A) NAME/KEY: misc_feature
79                  (B) LOCATION: 855..879
80
81       (ix) FEATURE:
82                  (A) NAME/KEY: CDS
83                  (B) LOCATION: 57..752
84
85
86       (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:
87
88  GTCGACTGGA ACGAGACGAC CTGCTCTGTC ACAGGCATGA GGGGTCCCCG GCAGAG        56
89
90  ATG ACA GTG CTG GCG CCA GCC TGG AGC CCA AAT TCC TCC CTG TTG CTG     104
91  Met Thr Val Leu Ala Pro Ala Trp Ser Pro Asn Ser Ser Leu Leu Leu
92   1               5                   10                  15
93
94  CTG TTG CTG CTG CTG AGT CCT TGC CTG CGG GGG ACA CCT GAC TGT TAC     152
95  Leu Leu Leu Leu Leu Ser Pro Cys Leu Arg Gly Thr Pro Asp Cys Tyr
96              20                  25                  30
97  TTC AGC CAC AGT CCC ATC TCC TCC AAC TTC AAA GTG AAG TTT AGA GAG     200
98  Phe Ser His Ser Pro Ile Ser Ser Asn Phe Lys Val Lys Phe Arg Glu
99              35                  40                  45
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RAW SEQUENCE LISTING
PATENT APPLICATION   *US/08/993,962*

INPUT SET: S3072.raw

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100
101    TTG ACT GAC CAC CTG CTT AAA GAT TAC CCA GTC ACT GTG GCC GTC AAT    248
102    Leu Thr Asp His Leu Leu Lys Asp Tyr Pro Val Thr Val Ala Val Asn
103        50                  55                  60
104
105    CTT CAG GAC GAG AAG CAC TGC AAG GCC TTG TGG AGC CTC TTC CTA GCC    296
106    Leu Gln Asp Glu Lys His Cys Lys Ala Leu Trp Ser Leu Phe Leu Ala
107    65                  70                  75                  80
108
109    CAG CGC TGG ATA GAG CAA CTG AAG ACT GTG GCA GGG TCT AAG ATG CAA    344
110    Gln Arg Trp Ile Glu Gln Leu Lys Thr Val Ala Gly Ser Lys Met Gln
111                85                  90                  95
112
113    ACG CTT CTG GAG GAC GTC AAC ACC GAG ATA CAT TTT GTC ACC TCA TGT    392
114    Thr Leu Leu Glu Asp Val Asn Thr Glu Ile His Phe Val Thr Ser Cys
115                100                 105                 110
116
117    ACC TTC CAG CCC CTA CCA GAA TGT CTG CGA TTC GTC CAG ACC AAC ATC    440
118    Thr Phe Gln Pro Leu Pro Glu Cys Leu Arg Phe Val Gln Thr Asn Ile
119            115                 120                 125
120
121    TCC CAC CTC CTG AAG GAC ACC TGC ACA CAG CTG CTT GCT CTG AAG CCC    488
122    Ser His Leu Leu Lys Asp Thr Cys Thr Gln Leu Leu Ala Leu Lys Pro
123        130                 135                 140
124
125    TGT ATC GGG AAG GCC TGC CAG AAT TTC TCT CGG TGC CTG GAG GTG CAG    536
126    Cys Ile Gly Lys Ala Cys Gln Asn Phe Ser Arg Cys Leu Glu Val Gln
127    145                 150                 155                 160
128
129    TGC CAG CCG GAC TCC TCC ACC CTG CTG CCC CCA AGG AGT CCC ATA GCC    584
130    Cys Gln Pro Asp Ser Ser Thr Leu Leu Pro Pro Arg Ser Pro Ile Ala
131                165                 170                 175
132
133    CTA GAA GCC ACG GAG CTC CCA GAG CCT CGG CCC AGG CAG CTG TTG CTC    632
134    Leu Glu Ala Thr Glu Leu Pro Glu Pro Arg Pro Arg Gln Leu Leu Leu
135                180                 185                 190
136
137    CTG CTG CTG CTG CTG CCT CTC ACA CTG GTG CTG CTG GCA GCC GCC TGG    680
138    Leu Leu Leu Leu Leu Pro Leu Thr Leu Val Leu Leu Ala Ala Ala Trp
139            195                 200                 205
140
141    GGC CTT CGC TGG CAA AGG GCA AGA AGG AGG GGG GAG CTC CAC CCT GGG    728
142    Gly Leu Arg Trp Gln Arg Ala Arg Arg Arg Gly Glu Leu His Pro Gly
143        210                 215                 220
144
145    GTG CCC CTC CCC TCC CAT CCC TAGGATTCGA GCCTTGTGCA TCGTTGACTC    779
146    Val Pro Leu Pro Ser His Pro
147    225                 230
148
149    AGCCAGGGTC TTATCTCGGT TACACCTGTA ATCTCAGCCC TTGGGAGCCC AGAGCAGGAT 839
150
151    TGCTGAATGG TCTGGAGCAG GTCGTCTCGT TCCAGTCGAC                       879
152
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153    (2) INFORMATION FOR SEQ ID NO:2:
154
155            (i) SEQUENCE CHARACTERISTICS:
156                  (A) LENGTH: 231 amino acids
157                  (B) TYPE: amino acid
158                  (D) TOPOLOGY: linear
159
160            (ii) MOLECULE TYPE: protein
161
162
163            (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:
164
165    Met Thr Val Leu Ala Pro Ala Trp Ser Pro Asn Ser Ser Leu Leu Leu
166     1               5                  10                  15
167
168    Leu Leu Leu Leu Leu Ser Pro Cys Leu Arg Gly Thr Pro Asp Cys Tyr
169               20                  25                  30
170
171    Phe Ser His Ser Pro Ile Ser Ser Asn Phe Lys Val Lys Phe Arg Glu
172           35                  40                  45
173
174    Leu Thr Asp His Leu Leu Lys Asp Tyr Pro Val Thr Val Ala Val Asn
175        50                  55                  60
176
177    Leu Gln Asp Glu Lys His Cys Lys Ala Leu Trp Ser Leu Phe Leu Ala
178    65                  70                  75                  80
179
180    Gln Arg Trp Ile Glu Gln Leu Lys Thr Val Ala Gly Ser Lys Met Gln
181               85                  90                  95
182
183    Thr Leu Leu Glu Asp Val Asn Thr Glu Ile His Phe Val Thr Ser Cys
184               100                 105                 110
185
186    Thr Phe Gln Pro Leu Pro Glu Cys Leu Arg Phe Val Gln Thr Asn Ile
187           115                 120                 125
188
189    Ser His Leu Leu Lys Asp Thr Cys Thr Gln Leu Leu Ala Leu Lys Pro
190        130                 135                 140
191
192    Cys Ile Gly Lys Ala Cys Gln Asn Phe Ser Arg Cys Leu Glu Val Gln
193    145                 150                 155                 160
194
195    Cys Gln Pro Asp Ser Ser Thr Leu Leu Pro Pro Arg Ser Pro Ile Ala
196               165                 170                 175
197
198    Leu Glu Ala Thr Glu Leu Pro Glu Pro Arg Pro Arg Gln Leu Leu Leu
199               180                 185                 190
200
201    Leu Leu Leu Leu Leu Pro Leu Thr Leu Val Leu Leu Ala Ala Ala Trp
202           195                 200                 205
203
204    Gly Leu Arg Trp Gln Arg Ala Arg Arg Arg Gly Glu Leu His Pro Gly
205           210                 215                 220
```

INPUT SET: S3072.raw

```
206
207    Val Pro Leu Pro Ser His Pro
208    225                 230
209
210         (2)  INFORMATION FOR SEQ ID NO:3:
211
212         (i)  SEQUENCE CHARACTERISTICS:
213              (A)  LENGTH: 24 base pairs
214              (B)  TYPE: nucleic acid
215              (C)  STRANDEDNESS: single
216              (D)  TOPOLOGY: linear
217
218      (iii) HYPOTHETICAL: NO
219
220       (iv) ANTI-SENSE: NO
221
222        (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:
223
224    TCGACTGGAA CGAGACGACC TGCT                                        24
225
226
227    (2)  INFORMATION FOR SEQ ID NO:4:
228
229         (i)  SEQUENCE CHARACTERISTICS:
230              (A)  LENGTH: 20 base pairs
231              (B)  TYPE: nucleic acid
232              (C)  STRANDEDNESS: single
233              (D)  TOPOLOGY: linear
234
235      (iii) HYPOTHETICAL: NO
236
237       (iv) ANTI-SENSE: NO
238
239        (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:
240
241    AGCAGGTCGT CTCGTTCCAG                                             20
242
243    (2)  INFORMATION FOR SEQ ID NO:5:
244
245         (i)  SEQUENCE CHARACTERISTICS:
246              (A)  LENGTH: 988 base pairs
247              (B)  TYPE: nucleic acid
248              (C)  STRANDEDNESS: single
249              (D)  TOPOLOGY: linear
250
251       (ii) MOLECULE TYPE: cDNA to mRNA
252
253      (iii) HYPOTHETICAL: NO
254
255       (iv) ANTI-SENSE: NO
256
257       (ix) FEATURE:
258              (A)  NAME/KEY: CDS
```

SEQUENCE VERIFICATION REPORT
PATENT APPLICATION *US/08/993,962*

INPUT SET: S3072.raw

Line	Error	Original Text
28	Wrong Classification	(C) CLASSIFICATION:435

SEQUENCE MISSING ITEM REPORT
PATENT APPLICATION   *US/08/993,962*

INPUT SET: S3072.raw

< < THERE ARE NO ITEMS MISSING > >